

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/926,084B  
Source: IFW/6  
Date Processed by STIC: 08-11-2005

# ***ENTERED***



1FW16

## RAW SEQUENCE LISTING

DATE: 08/11/2005

PATENT APPLICATION: US/09/926,084B

TIME: 15:04:31

Input Set : A:\213129USOPCT.txt

Output Set: N:\CRF4\08112005\I926084B.raw

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3 <110> APPLICANT: SYODA, MAKOTO
4     SUGANO, YASUSHI
5     KUBOTA, HIDETOSHI
7 <120> TITLE OF INVENTION: NOVEL ENZYME WITH DECOLORIZING ACTIVITY AND METHOD FOR
8     DECOLORIZING DYES BY USING THE SAME
10 <130> FILE REFERENCE: 213129USOPCT
12 <140> CURRENT APPLICATION NUMBER: US 09/926,084B
13 <141> CURRENT FILING DATE: 2001-08-27
15 <150> PRIOR APPLICATION NUMBER: JP 99/11-050562
16 <151> PRIOR FILING DATE: 1999-02-26
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 6
24 <212> TYPE: PRT
25 <213> ORGANISM: Geotrichum candidum
27 <400> SEQUENCE: 1
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30 1      5
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 8
35 <212> TYPE: PRT
36 <213> ORGANISM: Geotrichum candidum
38 <400> SEQUENCE: 2
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41 1      5
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 21
46 <212> TYPE: PRT
47 <213> ORGANISM: Geotrichum candidum
49 <400> SEQUENCE: 3
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55 Thr Ala Gln Asp Arg
56      20
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 21
61 <212> TYPE: PRT
62 <213> ORGANISM: Geotrichum candidum
64 <400> SEQUENCE: 4
66 Ser Gly Ala Pro Ile Asp Leu Ala Pro Thr Ala Asp Asp Pro Ala Leu
67 1      5      10      15
70 Gly Ala Asp Pro Gln

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77 <213> ORGANISM: Geotrichum candidum
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85 <210> SEQ ID NO: 6
86 <211> LENGTH: 6
87 <212> TYPE: PRT
88 <213> ORGANISM: Geotrichum candidum
90 <400> SEQUENCE: 6
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93 1          5
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 498
98 <212> TYPE: PRT
99 <213> ORGANISM: Geotrichum candidum
101 <400> SEQUENCE: 7
103 Met Asp Leu Ser Leu Phe Val Val Ser Val Ala Val Leu Val Gly Ser
104 1          5          10          15
107 Ser Ser His Val Asn Ala Ala Lys Leu Gly Ala Arg Gln Thr Arg Thr
108          20          25          30
111 Thr Pro Leu Leu Thr Asn Phe Pro Gly Gln Ala Pro Leu Pro Thr Leu
112          35          40          45
115 Thr Gln His Thr Thr Glu Ser Gly Ala Asn Asp Thr Ile Leu Pro Leu
116          50          55          60
119 Asn Asn Ile Gln Gly Asp Ile Leu Val Gly Met Lys Lys Gln Lys Glu
120 65          70          75          80
123 Arg Phe Val Phe Phe Gln Val Asn Asp Ala Thr Ser Phe Lys Thr Ala
124          85          90          95
127 Leu Lys Thr Tyr Val Pro Gln Arg Ile Thr Ser Ala Ala Ile Leu Ile
128          100          105          110
131 Ser Asp Pro Ser Gln Gln Pro Leu Ala Phe Val Asn Leu Gly Phe Ser
132          115          120          125
135 Asn Thr Gly Leu Gln Ala Leu Gly Ile Thr Asp Asp Leu Gly Asp Ala
136          130          135          140
139 Gln Phe Pro Asp Gly Gln Phe Ala Asp Ala Ala Asn Leu Gly Asp Asp
140 145          150          155          160
143 Leu Ser Gln Trp Val Ala Pro Phe Thr Gly Thr Thr Ile His Gly Val
144          165          170          175
147 Phe Leu Ile Gly Ser Asp Gln Asp Asp Phe Leu Asp Gln Phe Thr Asp
148          180          185          190
151 Asp Ile Ser Ser Thr Phe Gly Ser Ser Ile Thr Gln Val Gln Ala Leu
152          195          200          205
155 Ser Gly Ser Ala Arg Pro Gly Asp Gln Ala Gly His Glu His Phe Gly
156          210          215          220
159 Phe Leu Asp Gly Ile Ser Gln Pro Ser Val Thr Gly Trp Glu Thr Thr

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160 225          230          235          240
163 Val Phe Pro Gly Gln Ala Val Val Pro Pro Gly Ile Ile Leu Thr Gly
164          245          250          255
167 Arg Asp Gly Asp Thr Gly Thr Arg Pro Ser Trp Ala Leu Asp Gly Ser
168          260          265          270
171 Phe Met Ala Phe Arg His Phe Gln Gln Lys Val Pro Glu Phe Asn Ala
172          275          280          285
175 Tyr Thr Leu Ala Asn Ala Ile Pro Ala Asn Ser Ala Gly Asn Leu Thr
176          290          295          300
179 Gln Gln Glu Gly Ala Glu Phe Leu Gly Ala Arg Met Phe Gly Arg Trp
180 305          310          315          320
183 Lys Ser Gly Ala Pro Ile Asp Leu Ala Pro Thr Ala Asp Asp Pro Ala
184          325          330          335
187 Leu Gly Ala Asp Pro Gln Arg Asn Asn Asn Phe Asp Tyr Ser Asp Thr
188          340          345          350
191 Leu Thr Asp Glu Thr Arg Cys Pro Phe Gly Ala His Val Arg Lys Thr
192          355          360          365
195 Asn Pro Arg Gln Asp Leu Gly Gly Pro Val Asp Thr Phe His Ala Met
196          370          375          380
199 Arg Ser Ser Ile Pro Tyr Gly Pro Glu Thr Ser Asp Ala Glu Leu Ala
200 385          390          395          400
203 Ser Gly Val Thr Ala Gln Asp Arg Gly Leu Leu Phe Val Glu Tyr Gln
204          405          410          415
207 Ser Ile Ile Gly Asn Gly Phe Arg Phe Gln Gln Ile Asn Trp Ala Asn
208          420          425          430
211 Asn Ala Asn Phe Pro Phe Ser Lys Pro Ile Thr Pro Gly Ile Glu Pro
212          435          440          445
215 Ile Ile Gly Gln Thr Thr Pro Arg Thr Val Gly Gly Leu Asp Pro Leu
216          450          455          460
219 Asn Gln Asn Glu Thr Phe Thr Val Pro Leu Phe Val Ile Pro Lys Gly
220 465          470          475          480
223 Gly Glu Tyr Phe Phe Leu Pro Ser Ile Ser Ala Leu Thr Ala Thr Ile
224          485          490          495
227 Ala Ala
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 1494
233 <212> TYPE: DNA
234 <213> ORGANISM: Geotrichum candidum
236 <400> SEQUENCE: 8
237 atgcgcttgt cgctgtttgt cgtgtcggtt gccgtactcg tcgggtcgag ctgcgatgtc 60
239 aatgctgcta aactcggcgc gagacagacg cgtacgacac ccctcctcac taattttccg 120
241 ggacaagccc cgctgccgac tctaacgcag catacgactg agagcggggc caacgataca 180
243 attctgcccc tgaacaacat acaaggcgac attttggttg gcatgaagaa acagaaggaa 240
245 cgcttcgtct ttttccaagt caatgacgca acctcggtca agacggcggt gaagacctac 300
247 gtgcctgagc gcatcacgtc ggcggcgatt ttgatttcag atcctttctca gcagccgttg 360
249 gctttcgtca acctcggggt ttcgaacaca ggctccagg cgcttggaat taccgacgat 420
251 ctgggtgatg cacaattccc agatggtcag ttcgcagacg ccgcaaacct cggggacgac 480
253 ctccagccaat ggggtggcgcc ttttactggt accaccatcc atggtgtctt tctgattggt 540
255 aggcgaccag gacgacttct tggatcagtt cacggatgat atctcttcga cctttggttc 600

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257 tccatcactc aggtgcaggc gctcagtggt tctgcgcgtc caggagatca ggctgggtcat 660
259 gaacacttcg gggttcctcg cggcatctcg cagccctcag tcacaggctg ggagacgacc 720
261 gtcttccctg gacaggcggt cgtcccacct ggaattatcc tctctggacg cgatggggac 780
263 acgggcaccc gaccgtcgtg ggctctagat gggagtattca tggcattccg gcacttccag 840
265 cagaaggtcc ccgaattcaa cgcgtacacg ctgcgcaacg cgatacccg cgacagcgcg 900
267 ggaaacctca cccagcagga aggtgcagag ttcctcggcg cgcgcgtggt cggccgttg 960
269 aagagcgggc cgccgattga cctcgcgccc acggcggacg acccagcgct cggcgccgac 1020
271 ccgcagagga acaacaattt cgattactca gacacgctga cggacgagac gcgctgcccc 1080
273 ttcggtgcac acgtgaggaa gacgaaccct cgacaggacc tgggtggacc ggtcgacacc 1140
275 ttccacgcta tgcggtccag tatcccgtac ggcccagaaa cgtctgatgc agaacttgcg 1200
277 tcgggcgtga ctgcgcaaga ccgcggtctt cttttcgtcg agtaccagtc cattattggt 1260
279 aatgggttca gggtccagca gattaactgg gcgaacaatg cgaacttccc tttctccaaa 1320
281 ccgatcacgc ctggaattga gcctatcatc ggccagacga ctccacgcac tgtcggcggg 1380
283 ctcgaccccc tcaaccagaa tgagacgttc acagtaccgc tgtttgatgat cccgaagggc 1440
285 ggggaataact ttttcttgcc ctctatctct gcgctcactg cgactatcgc tgct 1494
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 26
290 <212> TYPE: PRT
291 <213> ORGANISM: Geotrichum candidum
294 <220> FEATURE:
295 <221> NAME/KEY: NON_CONS
296 <222> LOCATION: (13)..(14)
298 <400> SEQUENCE: 9
300 Gln Ala Pro Leu Pro Thr Leu Thr Gln His Thr Thr Glu Val Ala Pro
301 1 5 10 15
304 Phe Thr Gly Thr Thr Ile His Gly Val Phe
305 20 25
308 <210> SEQ ID NO: 10
309 <211> LENGTH: 26
310 <212> TYPE: PRT
311 <213> ORGANISM: Saccharomyces cerevisiae
314 <220> FEATURE:
315 <221> NAME/KEY: NON_CONS
316 <222> LOCATION: (13)..(14)
318 <400> SEQUENCE: 10
320 Gly Pro Val Leu Val Arg Leu Ala Trp His Thr Ser Gly Arg Glu Val
321 1 5 10 15
324 Val Ala Leu Met Gly Ala His Ala Leu Gly
325 20 25
328 <210> SEQ ID NO: 11
329 <211> LENGTH: 26
330 <212> TYPE: PRT
331 <213> ORGANISM: Escherichia coli
334 <220> FEATURE:
335 <221> NAME/KEY: NON_CONS
336 <222> LOCATION: (13)..(14)
338 <400> SEQUENCE: 11
340 Ala Gly Leu Phe Ile Arg Met Ala Trp His Gly Ala Gly Glu Thr Val
341 1 5 10 15

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344 Ala Leu Ile Ala Gly Gly His Thr Leu Gly
345          20          25
348 <210> SEQ ID NO: 12
349 <211> LENGTH: 26
350 <212> TYPE: PRT
351 <213> ORGANISM: Arthromyces ramosus
354 <220> FEATURE:
355 <221> NAME/KEY: NON_CONS
356 <222> LOCATION: (13)..(14)
358 <400> SEQUENCE: 12
360 Val Arg Lys Ile Leu Arg Ile Val Phe His Asp Ala Ile Asp Glu Val
361 1          5          10          15
364 Val Asp Leu Leu Ala Ala His Ser Leu Ala
365          20          25
368 <210> SEQ ID NO: 13
369 <211> LENGTH: 26
370 <212> TYPE: PRT
371 <213> ORGANISM: Phanerochaete
374 <220> FEATURE:
375 <221> NAME/KEY: NON_CONS
376 <222> LOCATION: (13)..(14)
378 <400> SEQUENCE: 13
380 Ala His Glu Val Ile Arg Leu Thr Phe His Asp Ala Ile Phe Glu Val
381 1          5          10          15
384 Val Ser Leu Leu Ala Ser His Thr Val Ala
385          20          25
388 <210> SEQ ID NO: 14
389 <211> LENGTH: 26
390 <212> TYPE: PRT
391 <213> ORGANISM: Phanerochaete chrysosporium
394 <220> FEATURE:
395 <221> NAME/KEY: NON_CONS
396 <222> LOCATION: (13)..(14)
398 <400> SEQUENCE: 14
400 Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ser Ile Leu Glu Leu
401 1          5          10          15
404 Val Trp Met Leu Ser Ala His Ser Val Ala
405          20          25
408 <210> SEQ ID NO: 15
409 <211> LENGTH: 26
410 <212> TYPE: PRT
411 <213> ORGANISM: Tunip
414 <220> FEATURE:
415 <221> NAME/KEY: NON_CONS
416 <222> LOCATION: (13)..(14)
418 <400> SEQUENCE: 15
420 Gly Ala Ser Ile Leu Arg Leu Phe Phe His Asp Cys Phe Arg Asp Met
421 1          5          10          15
424 Val Ala Leu Ser Gly Ala His Thr Ile Gly

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**VERIFICATION SUMMARY**

DATE: 08/11/2005

PATENT APPLICATION: **US/09/926,084B**

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Input Set : **A:\213129US0PCT.txt**

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